

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:27:49 ; Search time 2530.16 Seconds
(without alignments)
10849.659 Million cell updates/sec

Title: US-09-856-979-6
Perfect score: 1695
Sequence: 1 ccgcagatcctctgtgtga.....tccatcaagccgtcgcgatg 1695

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_estc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	187.4	11.1	948	17 AQ329933	AQ329933 nbxb0046A
c 2	178.8	10.5	668	17 BH878425	BH878425 hs82a08.b
c 3	87	5.1	331	9 AL371988	AL371988 MtBA47H04
c 4	85.8	5.1	415	17 BH885023	BH885023 hw55f08.b
c 5	82.2	4.8	120	17 BH416345	BH416345 1007047F0
c 6	78.6	4.6	654	14 BU014814	BU014814 QGJ8H09.Y

c 7	78.6	4.6	655	14 BQ854032	BQ854032 QGB22C16.
c 8	78.6	4.6	670	14 BU010172	BU010172 QGJ12K14.
c 9	78.6	4.6	712	14 BU000882	BU000882 QGG26E24.
c 10	78.6	4.6	732	14 BU012310	BU012310 QGJ1J08.Y
c 11	78.6	4.6	744	14 BU014761	BU014761 QGJ8E16.Y
c 12	78.6	4.6	745	14 BQ850661	BQ850661 QGB13D16.
c 13	78.6	4.6	750	14 BQ993006	BQ993006 QGF27F06.
c 14	78.6	4.6	762	14 BQ853513	BQ853513 QGB20L12.
c 15	78	4.6	512	12 BG462180	BG462180 947047F08
c 16	78	4.6	607	14 BQ294181	BQ294181 1091026G0
c 17	78	4.6	642	14 BU037560	BU037560 946140C06
c 18	77	4.5	756	14 BQ839445	BQ839445 WHE4166_B
c 19	76.8	4.5	546	12 BF421436	BF421436 FMI_8_G02
c 20	76.6	4.5	167	17 AG024921	AG024921 Oryza sat
c 21	76.2	4.5	653	9 AI162258	AI162258 A014P73U
c 22	76	4.5	523	10 AW011614	AW011614 ST22H09.P
c 23	75.6	4.5	728	13 BM157838	BM157838 NXLV_025
c 24	75.4	4.4	497	13 BI644131	BI644131 949022A11
c 25	75.4	4.4	603	10 BE590288	BE590288 SB36 Sugra
c 26	75.4	4.4	625	12 BE942189	BE942189 EST421768
c 27	75.4	4.4	626	14 BU036825	BU036825 946130A04
c 28	75.4	4.4	629	12 BE942188	BE942188 EST421767
c 29	75.2	4.4	523	13 BI127466	BI127466 G061P11Y
c 30	75.2	4.4	555	10 BE499732	BE499732 WHE0975_G
c 31	75.2	4.4	561	13 BM188325	BM188325 saj99d11.
c 32	75.2	4.4	642	10 BE229756	BE229756 98SN0144
c 33	75.2	4.4	660	14 BQ294680	BQ294680 WHE2853_B
c 34	74.8	4.4	337	12 BF145411	BF145411 WHE1841-1
c 35	74.8	4.4	344	9 AJ499862	AJ499862 AJ499862
c 36	74.8	4.4	869	12 BG345098	BG345098 HVSMEG001
c 37	74.4	4.4	600	14 BQ149587	BQ149587 NF106B02F
c 38	73.8	4.4	406	10 BE407080	BE407080 WHE0448_9
c 39	73.8	4.4	512	10 AW282484	AW282484 LGL_313_B
c 40	73.8	4.4	570	10 AV933056	AV933056 AV933056
c 41	73.8	4.4	582	10 AV932088	AV932088 AV932088
c 42	73.8	4.4	592	10 AV934263	AV934263 AV934263
c 43	73.8	4.4	666	13 BJ472315	BJ472315 BJ472315
c 44	73.8	4.4	941	14 BM817125	BM817125 HCL10B06_
c 45	73.8	4.4	1116	11 AY103934	AY103934 zea mays

ALIGNMENTS

RESULT 1
AQ329933/c 948 bp DNA linear GSS 08-JAN-1999
LOCUS nbxb0046A15r CUGI Rice BAC Library Oryza sativa genomic clone
DEFINITION nbxb0046A15r, DNA sequence.
ACCESSION AQ329933
VERSION AQ329933.1 GI:4121783
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 948)
AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 96.
Location/Qualifiers 1..948

FEATURES

source

REFERENCE AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.			
TITLE	1 (bases 1 to 120)			
JOURNAL	Walbot,V.			
COMMENT	Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1007047 column: 14 Class: transposon-tagged.			
FEATURES	source	Location/Qualifiers		
	1..120	/organism="Zea mays" /cultivar="mixed background W23/A188/B73" /db_xref="taxon:4577" /clone_lib="1007 - RescueMu Grid H" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."		
BASE COUNT	25 a	25 c	33 g	37 t
ORIGIN				
Query Match	4.8%;	Score 82.2;	DB 17;	Length 120;
Best Local Similarity	80.7%;	Pred. No. 6.2e-13;		
Matches	96;	Conservative	0;	Mismatches 23; Indels 0; Gaps 0;
QY	382	TCTTCAGATCCCTTCCACATGCAATGTCGTAAGAACAGATACAGTGACGTTAGTTGT	441	
Db	2	TCTTCAGATCCCTCCCGCATGCAATGTCATAAAGGCAGACTCGGTGTGTGCCAGTTGT	61	
QY	442	AATGGACGGTCAATGCCATTTCTCTGAAGGCATGTTCCAGAGATGATGATTCTGGGATC	500	
Db	62	AATGGATGATCTGTGCTGTTTGTTCGGAAGGCATGCTCAGAGATGATCACTTCTGGGATC	120	
RESULT 6				
BU014814/c				
LOCUS	BU014814	654 bp	mRNA	linear EST 22-AUG-2002
DEFINITION	QGJ8H09.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone			
ACCESSION	QGJ8H09, mRNA sequence.			
VERSION	BU014814.1 GI:22449209			
KEYWORDS	EST.			
SOURCE	Lactuca sativa.			
ORGANISM	Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.			
REFERENCE	1 (bases 1 to 654)			
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavellie,D., Chevalier,P., Ziegler,J., Ellison P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.			

TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik (R.W.Michelmore) Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig7857, see http://cgpdb.ucdavis.edu/ for details. Plate: QGJ8 row: H column: 09.			
JOURNAL				
COMMENT				
FEATURES	source	Location/Qualifiers		
	1..654	/organism="Lactuca sativa" /cultivar="L.serriola" /db_xref="taxon:4236" /clone="QGJ8H09" /clone_lib="QG_EFGHJ lettuce serriola" /lab_host="E.coli" /note="Vector: pBRCNASf1AB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/ TAG_LIB=QG_EFGHJ lettuce serriola TAG_TISSUE=flowers pre-fertilized TAG_SEQ=GCCTGACGGG"		
BASE COUNT	162 a	151 c	152 g	189 t
ORIGIN				
Query Match	4.6%;	Score 78.6;	DB 14;	Length 654;
Best Local Similarity	60.6%;	Pred. No. 1.6e-11;		
Matches	129;	Conservative	0;	Mismatches 84; Indels 0; Gaps 0;
QY	614	GGAATAAAGCTAATACCTGTCCAAGAGTGGTGGCGCATTTGACCAATGAAGATCACAA	673	
Db	505	GGAACCTTGGTGGAGACTTGTTCATGAAGCTTTCGGCATTTGGACCACAGGAAAGGACTG	446	
QY	674	GCATGGCAAGAATGGCAATCTGGCAAGGAGCGGAATATATATTCTACTACATCGA	733	
Db	445	CTAGAGCTAAGATTAGAGCTATGGCATACTAGTGTAAAGTAGTATTAACCAACTCAA	386	
QY	734	ACAGGACCATATCAATGTGTCCTCCACCAAGGACCCCGCAGATAAGTTCCTGTTCTCC	793	
Db	385	AAAGCACCATATCAATGTGGCAACCCGAGCACACAGCAGAAACCTTCTTGCTCTCC	326	
QY	794	ACAGCAGAATATCCGCAACTGCATAGCTCCCAA	826	
Db	325	AGAGGAAGATATCAGCAGGTTTGGCCGCTCCTA	293	
RESULT 7				
BU054032/c				
LOCUS	BQ854032	655 bp	mRNA	linear EST 14-AUG-2002
DEFINITION	QG822C16.yg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone			
ACCESSION	QG822C16, mRNA sequence.			
VERSION	BQ854032.1 GI:22239497			
KEYWORDS	EST.			
SOURCE	Lactuca sativa.			
ORGANISM	Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.			
REFERENCE	1 (bases 1 to 655)			
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,			

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100

100

100

100